

FIGURE 1A

1 GAGGGTGAAGCCGGGTCTCGCGGCCGGGGCGCATGACTCCTCTCTGCCCTCAATTG 60  
61 CTCTGTCTCCTCGAGACCTGTACCCAGGGGTGCAAGGAACCCCATGGCTTGCAATGG 120  
121 CAGTGGGCCAGGGGCACTTTGACCCCTGAGGACTTGAACCTGACTGACGAGGCACTGAG 180  
181 ACTCAAGTACCTGGGGCCCCAGCAGACAGAGCTGTTCATGCCCATCTGTGCCACATACCT 240  
241 GCTGATCTTCGTGGTGGGCGCTGTGGGCAATGGGCTGACCTGTCTGGTCATCCTGCGCCA 300  
301 CAAGGCCATGCGCACGCCCTACCAACTACTACCTCTTCAGCCTGGCCCGTGTGCGGACCTGCT 360  
361 GGTGCTGCTGGTGGGCCCTGCCCTGGAGCTCTATGAGATGTGGCACAACTACCCCTTCCT 420  
421 GCTGGGCGTTGGTGGCTGCTATTTCGCGCACGCTACTGTTTGAGATGGTCTGCGCTGGCCTC 480  
481 AGTGCTCAACGTCACTGCCCTGAGCGTGGAACGCTATGTGGCCGTGGTGCACCCACATCCA 540  
541 GGCCAGGTCCATGGTGACGCGGGCCCATGTGCGCCGAGTGCTTGGGGCCGCTCTGGGGTCT 600  
601 TGCCATGCTCTGCTCCCTGCCCAACACACGCTGCACGGCATCCGGCAGCTGCACGTGCC 660  
661 CTGCCCCGGGCCAGTGCCAGACTCAGCTGTTTGCACTGCTGGTCCGCCCCACGGGCCCTCTA 720

10



FIGURE 2A

1	M	T	P	L	C	L	N	C	S	V	L	P	G	D	L	Y	P	G	G	A	20
21	R	N	P	M	A	C	N	G	S	A	A	R	G	H	F	D	P	E	D	L	40
41	N	L	T	D	E	A	L	R	L	K	Y	L	G	P	Q	Q	T	E	L	F	60
61	M	P	I	C	A	T	Y	L	L	I	F	V	V	G	A	V	G	N	G	L	80
81	T	C	L	V	I	L	R	H	K	A	M	R	T	P	T	N	Y	Y	L	F	100
101	S	L	A	V	S	D	L	L	V	L	L	V	G	L	P	L	E	L	Y	E	120
121	M	W	H	N	Y	P	F	L	L	G	V	G	G	C	Y	F	R	T	L	L	140
141	F	E	M	V	C	L	A	S	V	L	N	V	T	A	L	S	V	E	R	Y	160
161	V	A	V	V	H	P	L	Q	A	R	S	M	V	T	R	A	H	V	R	R	180
181	V	L	G	A	V	W	G	L	A	M	L	C	S	L	P	N	T	S	L	H	200
201	G	I	R	Q	L	H	V	P	C	R	G	P	V	P	D	S	A	V	C	M	220
221	L	V	R	P	R	A	L	Y	N	M	V	V	O	T	T	A	L	L	F	F	240

— 22 —

100

**Abstract**

FIGURE 3A

1 AGGGGAGGCTCAGGCCTTGGATTTTAATGTCAGGGATGGA~~AA~~AACTTCAGAAATGCTTCCT 60  
61 GGATCTACGACAGAACTAGAGATCCATTCCAGAAACACCTGAACAGCACCGAGGAGT 120  
121 ATCTGGCCTTCCTCTGCGGACCTCGGCGCAGCCACTTCTTCCCTCCCCGTGTCTGTGTGTGT 180  
181 ATGTGCCAATTTTGTGGTGGGGGTCAATTGGCAATGTCCCTGGTGTGCCCTGGTGATTCTGC 240  
241 AGCACGAGCTATGAAGACGCCCACTACTACCTCTTTCAGCCCTGGCGGTCTCTGACC 300  
301 TCCTGGTCCCTGCTCCTTGGAATGCCCCCTGGAGGTCTATGAGATGTGGCGCAACTACCCCTT 360  
361 TCTTGTTCGGGCCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTTGAGACCCGTGTGCTTCG 420  
421 CCTCCATCCTCAGCATCACCAACCGTCAGCGTGGAGCGCTACGTGGCCATCCTACACCCGT 480  
481 TCCGCGCCAAACTGCAGAGACCCGGCGCCCGCCCTCAGGATCCTCGGCATCGTCTGGG 540  
541 GCTTCTCCGTGCTCTTCTCCCTGCCCAACACACGCAATCCATGGCATCAAGTTCCACTACT 600  
601 TCCCCAATGGGTCCCTGGTCCCAGGTTCCGGCCACCTGTACGGTCATCAAGCCCCATGTGGA 660  
661 TCTACAATTTCAATCATCCAGGTCACCTCCTTCCCTATTCTACCTCCTCCCCCATGACTGTCA 720

## FIGURE 3B

721 TCAGTGTCTCTACTACCTCATGGCACTCAGACTAAAGAAAGACAAATCTCTTGAGGCAG 780  
781 ATGAAGGGAATGCAAAATATTCAAAGACCCCTGCAGAAAATCAGTCAACAAGATGCTGTTG 840  
841 TCTTGGTCTTAGTGTTTGCTATCTGTTGGGCCCCCGTTCCACATGACCGACTCTTCTTCA 900  
901 GCTTTGTGGAGGAGTGGAGTGAATCCCTGGCTGCTGTGTTCAACCTCGTCCATGTGGTGT 960  
961 CAGGTGCTTCTTCTACCTGAGCTCAGCTGTCAACCCCATTTATATAACCTACTGTCTC 1020  
1021 GCCGCTTCCAGGCAGCATTCAGAAATGTGATCTCTTCTTTCCACAAACAGTGGCACTCCC 1080  
1081 AGCATGACCCACAGTTGCCACCTGCCCCAGCGGAACATCTTCCGTGACAGAATGCCACTTTG 1140  
1141 TGGAGCTGACCGAAGATATAGGTCCCCCAATTCCCCATGTCTCAGTCAATGCACAACCTCTC 1200  
1201 ACCTCCCAACAGCCCCTCTCTAGTGAACAGATGTCAAGAACAACTATCAAGCTTCCACT 1260  
1261 TTAACAAAACCTGAATTTTCAGAGCTGACTCTCCCTC 1298

## FIGURE 4A

1 M S G M E K L Q N A S W I Y Q Q K L E D 20  
21 P F Q K H L N S T E E Y L A F L C G P R 40  
41 R S H F F L P V S V V Y V P I F V V G V 60  
61 I G N V L V C L V I L Q H Q A M K T P T 80  
81 N Y Y L F S L A V S D L L V L L L G M P 100  
101 L E V Y E M W R N Y P F L F G P V G C Y 120  
121 F K T A L F E T V C F A S I L S I T T V 140  
141 S V E R Y V A I L H P F R A K L Q S T R 160  
161 R R A L R I L G I V W G F S V L F S L P 180  
181 N T S I H G I K F H Y F P N G S L V P G 200  
201 S A T C T V I K P M W I Y N F I I Q V T 220  
221 S F L F Y L L P M T V I S V L Y Y L M A 240

## FIGURE 4B

241	L	R	L	K	K	D	K	S	L	E	A	D	E	G	N	A	N	I	Q	R	260
261	P	C	R	K	S	V	N	K	M	L	F	V	L	V	L	V	F	A	I	C	280
281	W	A	P	F	H	I	D	R	L	F	F	S	F	V	E	E	W	S	E	S	300
301	L	A	A	V	F	N	L	V	H	V	V	S	G	V	F	F	Y	L	S	S	320
321	A	V	N	P	I	I	Y	N	L	L	S	R	R	F	Q	A	A	F	Q	N	340
341	V	I	S	S	F	H	K	Q	W	H	S	Q	H	D	P	Q	L	P	P	A	360
361	Q	R	N	I	F	L	T	E	C	H	F	V	E	L	T	E	D	I	G	P	380
381	Q	F	P	C	Q	S	S	M	H	N	S	H	L	P	T	A	L	S	S	E	400
401	Q	M	S	R	T	N	Y	Q	S	F	H	F	N	K	T						415



FIGURE 5

1 MTPLCLNCSVLPGLDLYPGGARNPMACNGSAARGHFDP..EDLNLTDEALR 48  
 1 .....MSGMEKLQNASWIYQOKLEDPFQKHLNSTEEYLA 34  
 49 LKYLGPQQTELFMPICATYLLIFVVGAVGNGLTCLVILRHKAMRTPTNYY 98  
 35 F.LCGPRRSHFFLPVSVVYVPIFVVGVIGNVLVCLVILQHQAAMKTPTNYY 83  
 99 LFSLAVSDDLVLVLLVGLPLELYEMWHNYPFLLGVGGCYFRTLLFEMVCLAS 148  
 84 LFSLAVSDDLVLVLLGMPLEVEYEMWRNYPFLFGPVGVCYFKTALFETVCFAS 133  
 149 VLNVTALSVERYVAVVHPLQARSMVTRAHVRRLGAVWGLAMLCSLPNTS 198  
 134 ILSITTVSVERYVAILHPPFRAKLQSTRRALRILGIVWGFSLVFLSLPNTS 183  
 199 LHGIRQLHVPCRGVPDSAVCMLVRPRALYNMVVQTTALLFFCLPMAIMS 248  
 184 IHGIKFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYLLPMTVIS 233  
 249 VLYLLIGLRLRRERLLLMQEAKGRGSAAARSRYTCRLQQHDRGRRQVTKM 298  
 234 VLYYLMALRLKKDKSLEADEGN.....ANIQRPC.....RKSVMNKM 269  
 299 LFVLVVVFGICWAPFHADRVMSVVSQWTDGLHLAFQHVHVISGIFFYLG 348  
 270 LFVLVLVFAICWAPFHIDRLFFSFVEEWSESAAVFNLVHVVSQVFFYLS 319  
 349 SAANPVLYSLMSSRFRETFOEAL.CLGACCH.....RLRPRHSSHSLSRM 392  
 320 SAVNPIIYNLLSRRFQAQFQNVISSFHKQWHSQHDPQLPPAQORNIFLTEC 369  
 393 TTGSTLCDVGSLGSWVHPLAGNDGPEAQQETDPS..... 426  
 370 HFVELTEDIGPQFPCQSSMHNHLPTALSSEQMSRTNYQSFHFNKT 415

00609145-0630000

FIGURE 6

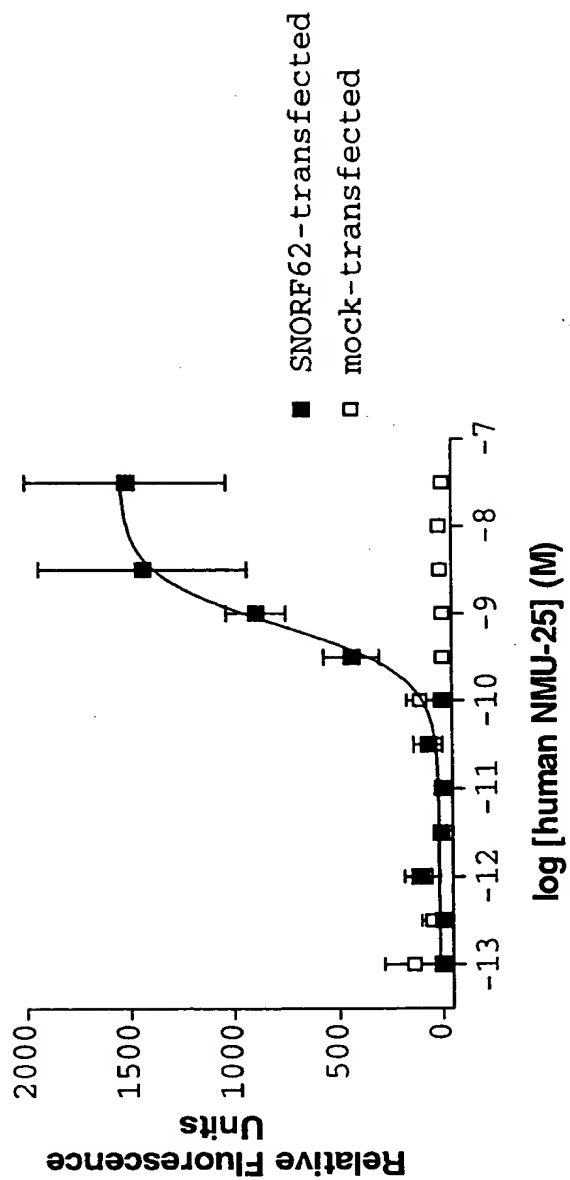


FIGURE 7

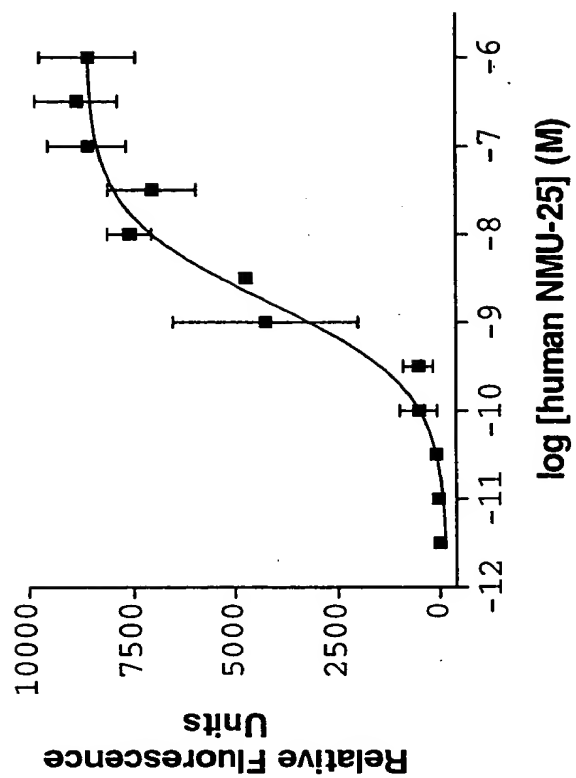
SNORF72-transfected COS-7  
cells

FIGURE 8

SNORF72-transfected COS-7 cells

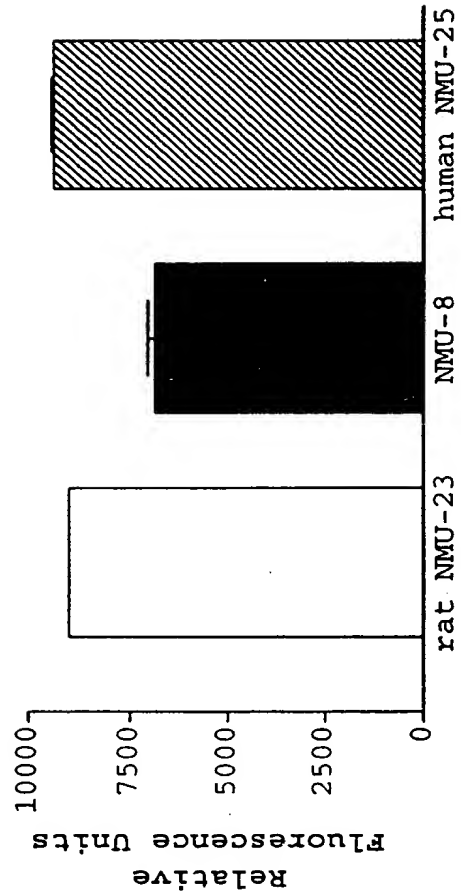


FIGURE 9A

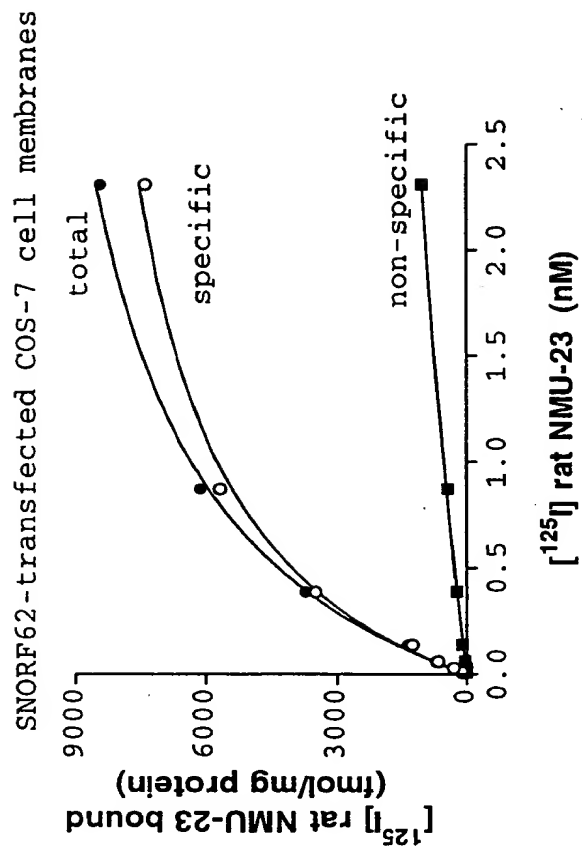


FIGURE 9B

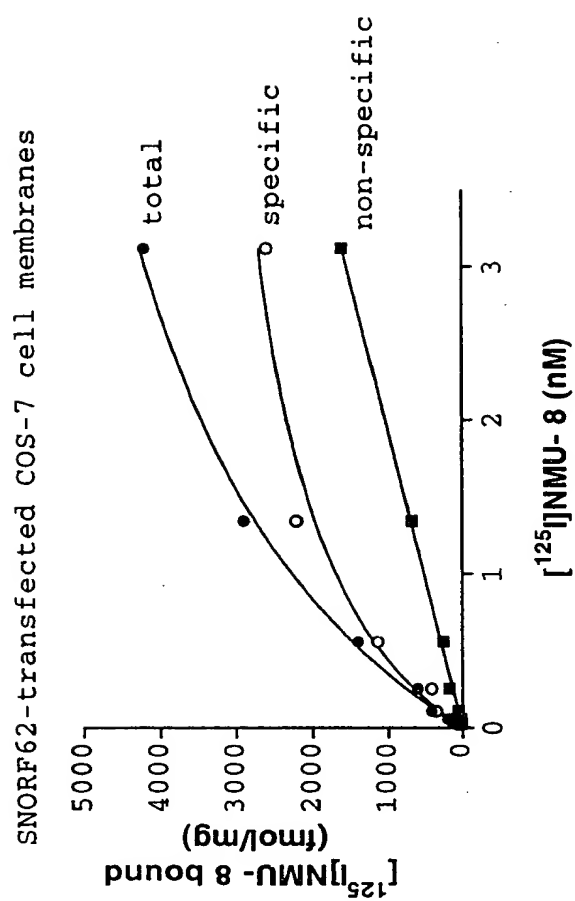


FIGURE 10

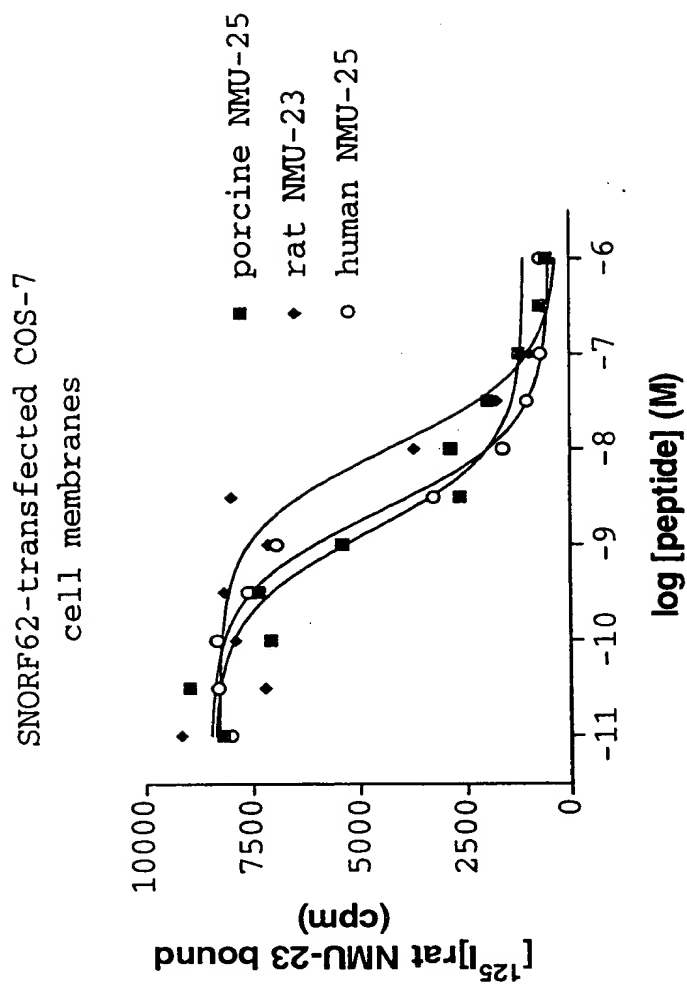


FIGURE 11A

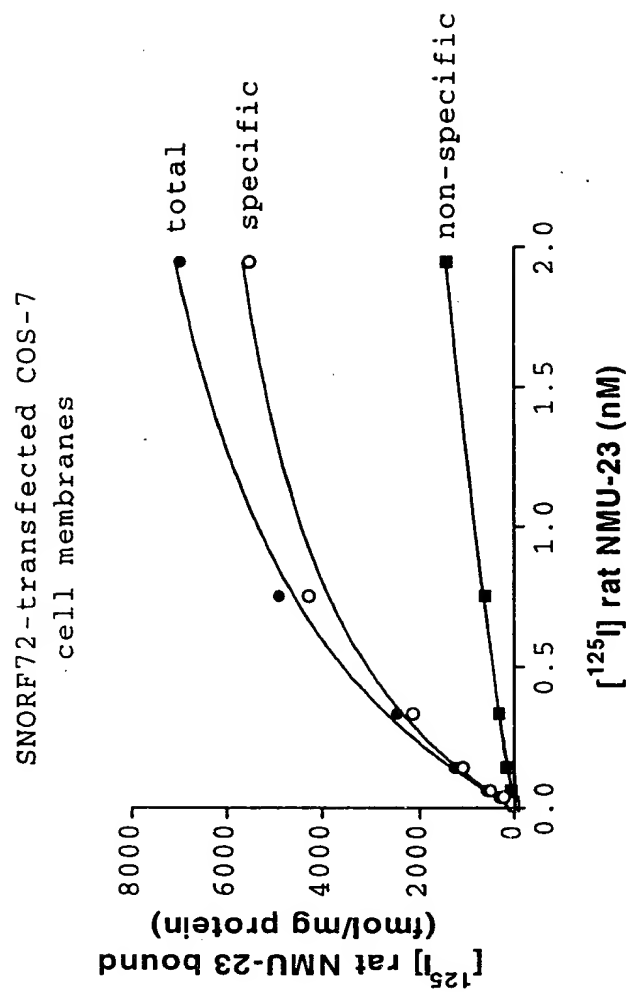




FIGURE 11B

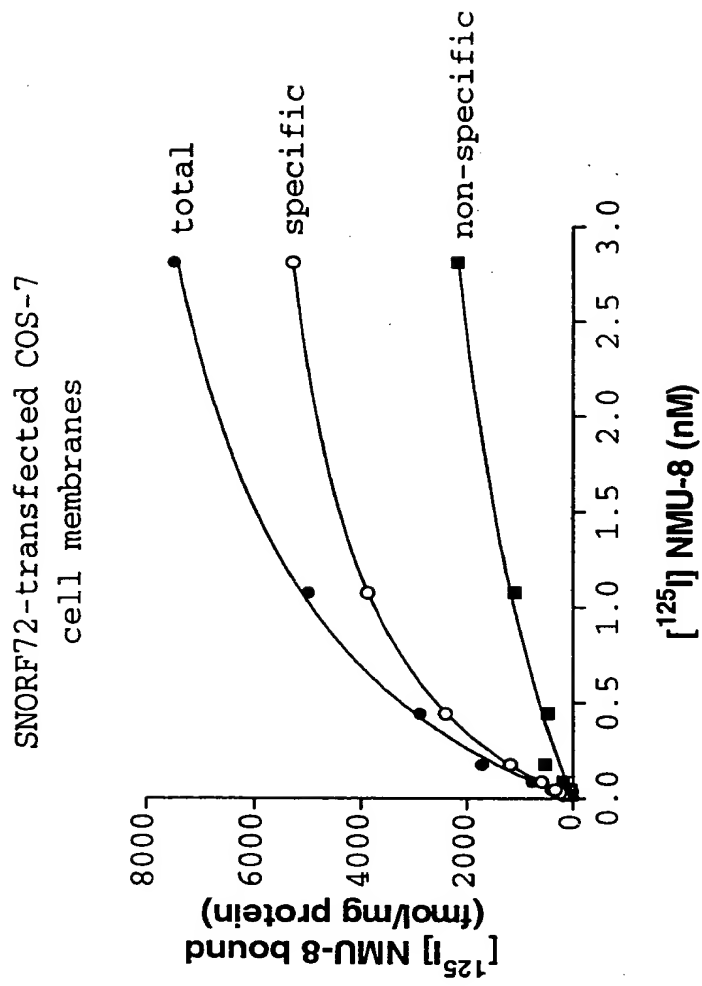


FIGURE 12

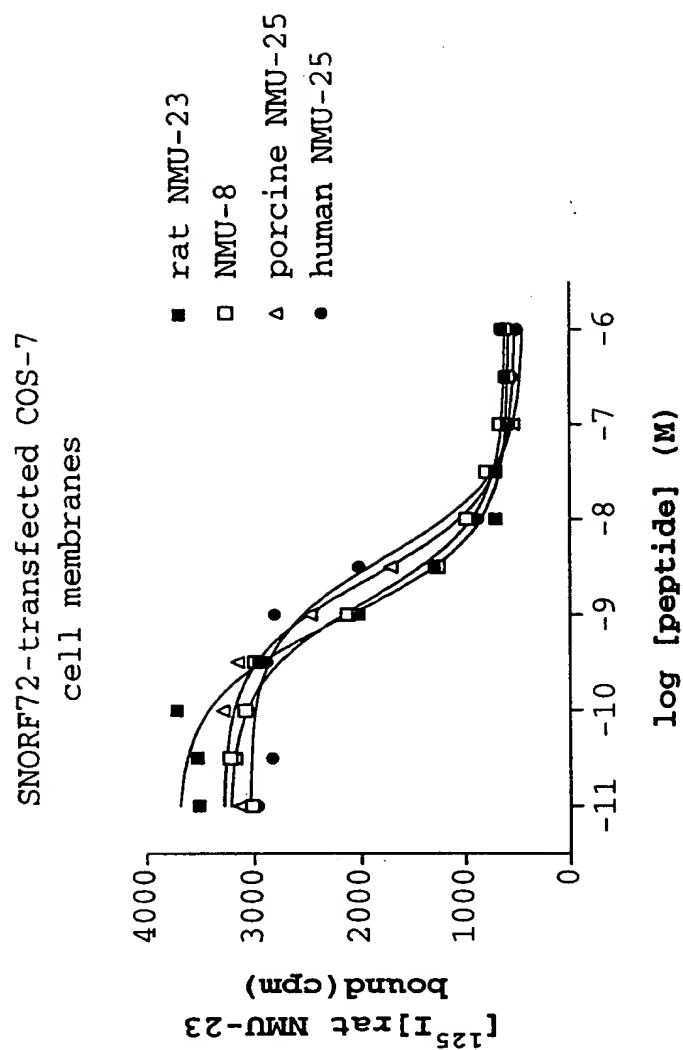


FIGURE 13

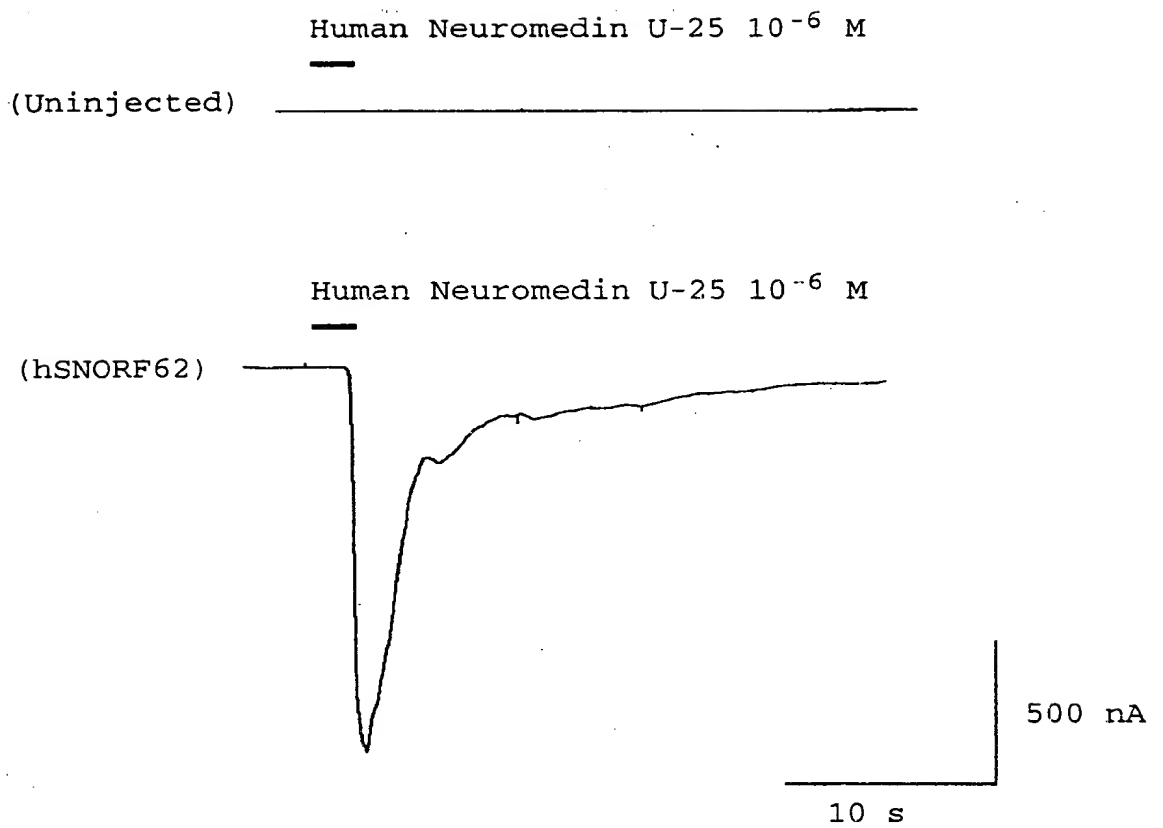


FIGURE 14A

1 GTTGTGGATTTTAAGCTCAGTAATGGGAAACTTGAAAAATGCTTCCTGGATCCACGATCC 60  
61 TCTCATGAAGTACTTGAACAGCACAGAGGAGTACTTGGCCCCACCTGTGTGGACCCAAAGCG 120  
121 CAGTGACCTATCCCTTCCGGTGTCTGTGGCCTATGCGCTGATCTTCCCTGGTGGGGTAAT 180  
181 GGGCAATCTTCTGGTGTGCATGGTGATTTGCCGACATCAGACTTTGAAGACACCCACCAA 240  
241 CTAATACTCTTCAGCTTGGCAGTCTCAGATCTGCTGGTCCCTGCTCTTGGGGATGCCTCT 300  
301 GGAAATCTACGAGATGTGGCACAAATTACCCCTTTCCCTGTTCCGGGCCCTGTGGGATGCTACTT 360  
361 CAAGACAGCCCTCTTCGAGACTGTGTGCTTTGGCCTCCATTTCTCAGTGTCAACACGGTTAG 420  
421 CGTAGAGCGCTATGTGGCCATTGTCCACCCCTTTCCGAGCCCAAGCTGGAGAGCACGCGGCG 480  
481 ACGGGCCCTCAGGATCCTCAGCCTAGTCTGGAGCTTCTCTGTGGTCTTTTCTTTGCCCAA 540  
541 TACCAGCATCCATGGCATCAAAGTTCAGCACATTTCCCAACGGGTCTCCGTACCTGGCTC 600  
601 AGCCACCTGCACAGTCACCAAACCCATGTGGGTGTATAACTTGATCATCCAAGCTACCAG 660  
661 CTTCCCTCTTACATCCTCCCAATGACCCCTCATCAGCGTCCCTCTACTACCTCATGGGGCT 720

FIGURE 14B

721 CAGGCTGAAGAGAGATGAATCCCTTGAGGCCAACAAGTGGCTGTGAATATTCACAGACC 780  
781 CTCTAGAAAGTCAGTCACCAAGATGCTGTTTGTCCTTGGTCCTCGTGTTCGTCATCTGCTG 840  
841 GACCCCTTCCATGTGGACCGGCTCTTCTTCAGCTTTGTGGAAGAGTGGACAGAGTCCCT 900  
901 GGCTGCTGTGTTCAACCTCATCCATGTGTATCAGGTGCTTCTTTTATCTGAGCTCCGC 960  
961 GGTCAACCCCATTAATCTATAACCTCCTGTCTCGGCGCTTCCGGCGGCCCTTTCGAAATGT 1020  
1021 TGTCTCCCCCTACCTGCAAAATGGTGCCATCCCCGGCATCGGCCACAGGGACCTCCAGCCCA 1080  
1081 GAAGATCATCTTCTTGACAGAAATGTCAACCTCGTGGAGCTGACAGAGGATGCAGGCCCCCA 1140  
1141 GTTCCCTGGTCAGTCATCCATCCACAACCAACCTTACCACGGCCCCCTGTGCAGGAGA 1200  
1201 GGTACCATAAAGGAGTGGTCAGAAGGCCTC 1231

1	M	G	K	L	E	N	A	S	W	I	H	D	P	L	M	K	Y	L	N	S	20
21	T	E	E	Y	L	A	H	L	C	G	P	K	R	S	D	L	S	L	P	V	40
41	S	V	A	Y	A	L	I	F	L	V	G	V	M	G	N	L	L	V	C	M	60
61	V	I	V	R	H	Q	T	L	K	T	P	T	N	Y	Y	L	F	S	L	A	80
81	V	S	D	L	L	V	L	L	L	G	M	P	L	E	I	Y	E	M	W	H	100
101	N	Y	P	F	L	F	G	P	V	G	C	Y	F	K	T	A	L	F	E	T	120
121	V	C	F	A	S	I	L	S	V	T	T	V	S	V	E	R	Y	V	A	I	140
141	V	H	P	F	R	A	K	L	E	S	T	R	R	R	A	L	R	I	L	S	160
161	L	V	W	S	F	S	V	V	F	S	L	P	N	T	S	I	H	G	I	K	180
181	F	Q	H	F	P	N	G	S	S	V	P	G	S	A	T	C	T	V	T	K	200
201	P	M	W	V	Y	N	L	I	I	Q	A	T	S	F	L	F	Y	I	L	P	220
221	M	T	L	I	S	V	L	Y	Y	L	M	G	L	R	L	K	R	D	E	S	240

FIGURE 15B

241	L	E	A	N	K	V	A	V	N	I	H	R	P	S	R	K	S	V	T	K	260
261	<u>M</u>	<u>L</u>	<u>F</u>	<u>V</u>	<u>L</u>	<u>V</u>	<u>L</u>	<u>V</u>	<u>F</u>	<u>A</u>	<u>I</u>	<u>C</u>	<u>W</u>	<u>T</u>	<u>P</u>	<u>F</u>	<u>H</u>	<u>V</u>	<u>D</u>	<u>R</u>	280
281	L	F	F	S	F	V	E	E	W	T	E	S	L	A	A	V	F	N	L	I	300
301	<u>H</u>	<u>V</u>	<u>V</u>	<u>S</u>	<u>G</u>	<u>V</u>	<u>F</u>	<u>F</u>	<u>Y</u>	<u>L</u>	<u>S</u>	<u>S</u>	<u>A</u>	<u>V</u>	<u>N</u>	<u>P</u>	<u>I</u>	<u>I</u>	<u>Y</u>	<u>N</u>	320
321	<u>L</u>	<u>L</u>	<u>S</u>	<u>R</u>	<u>R</u>	<u>F</u>	<u>R</u>	<u>A</u>	<u>A</u>	<u>F</u>	<u>R</u>	<u>N</u>	<u>V</u>	<u>V</u>	<u>S</u>	<u>P</u>	<u>T</u>	<u>C</u>	<u>K</u>	<u>W</u>	340
341	C	H	P	R	H	R	P	Q	G	P	P	A	Q	K	I	I	F	L	T	E	360
361	C	H	L	V	E	L	T	E	D	A	G	P	Q	F	P	G	Q	S	S	I	380
381	H	N	T	N	L	T	T	A	P	C	A	G	E	V	P	*					395

FIGURE 16A

SNORF72_RAT	~~~~~	~~~~~M	GKLENASWIH	....DPLMK	YLNSTEEYLA
SNORF72_HUMAN	~~~~~	~~~~~MSGM	EKLQNASWIY	QOKLEDPPQK	HLNSTEEYLA
SNORF62_HUMAN	MTPLCLNCSV	LPGDLYPGGA	RNPMACNGSA	ARGHFDP..E	DLNLTDEALR
SNORF72_RAT	H.LCGPKRSD	LSLPVSVAYA	LIFLVGMGN	LLVCMVIVRH	QTLKTPTNYY
SNORF72_HUMAN	F.LCGPRRSH	FFLPVSVVYV	PIFVGVIGN	VLVCLVILQH	QAMKTPTNYY
SNORF62_HUMAN	LKYLGPQQTE	LFMPICATYL	LIFVGAVERN	GLTCLVILRH	KAMRTPTNYY
SNORF72_RAT	LFSLAVSDLL	VLLLGMPLEI	YEMWHNYPFL	FGPVGCYFKT	ALFETVCFAS
SNORF72_HUMAN	LFSLAVSDLL	VLLLGMPLEV	YEMWRNYPFL	FGPVGCYFKT	ALFETVCFAS
SNORF62_HUMAN	LFSLAVSDLL	VLLVGLPLEL	YEMWHNYPFL	LGVGGCYFRT	LLFEMVCLAS
SNORF72_RAT	ILSVTTVSVE	RYVAIVHPFR	AKLESTRRRA	LRILSLVWSF	SVVFSLPNTS
SNORF72_HUMAN	ILSITTVSVE	RYVAILHPFR	AKLQSTRRRA	LRILGIVWGF	SVLFSLPNTS
SNORF62_HUMAN	VLNVTALSVE	RYVAVVHPLQ	ARSMVTRAHV	RRVLGAVWGL	AMLCSLPNTS
SNORF72_RAT	IHGKFKQHFP	NGSSVPGSAT	CTVTKPMWVY	NLIQATSFL	FYILPMTLIS
SNORF72_HUMAN	IHGKFKHYFP	NGSLVPGSAT	CTVIKPMWIY	NFIIQVTSFL	FYLLPMTVIS
SNORF62_HUMAN	LHGIRQLHVP	CRGPVPDSAV	CMLVRPRALY	NMVVQTALL	FFCLPMAIMS



FIGURE 16B

SNORF72_RAT	VLYYLMGLRL	KRDESL...E	A...NKVAVN	IHRPS.....	...RKSVTKM
SNORF72_HUMAN	VLYYLMALRL	KKDKSL...E	A...DEGNAN	IQRPC.....	...RKS VNKM
SNORF62_HUMAN	VLYLLIGLRL	RRERLLMQE	AKGRGSAAR	SRYTCRLQQH	DRGRRQVTKM
SNORF72_RAT	LFVLVLVFAI	CWTPFHVDRL	FFSFVEEWE	SLAAVFNLIH	VVSGVFFYLS
SNORF72_HUMAN	LFVLVLVFAI	CWAPFHIDRL	FFSFVEEWE	SLAAVFNLVH	VVSGVFFYLS
SNORF62_HUMAN	LFVLVVVFGI	CWAPFHADRV	MWSVVSQWTD	GLHLAFQHVH	VISGIFFFYLG
SNORF72_RAT	SAVNPIIYNL	LSRRFRAAFR	NV..VSPTCK	WCHPRHRPQG	PPAQKIIFLT
SNORF72_HUMAN	SAVNPIIYNL	LSRRFQAAFQ	NV..ISSFHK	QWHSQHDPQL	PPAQRNIFLT
SNORF62_HUMAN	SAANPVLVSL	MSSRFRETFQ	EALCLGACCH	RLRPRHSSH.	SLSRMTTGST
SNORF72_RAT	ECHLVELTED	AGPQFPGQSS	IHNTNLTAP	CAGEVP~~~~~	~~~~~
SNORF72_HUMAN	ECHFVELTED	IGPQFPCQSS	MHNSHLPTAL	SSEQMSRTNY	QSFHFNKT
SNORF62_HUMAN	LCDVGSLGSW	VHPLAGNDGP	EAQQETDPS~	~~~~~	~~~~~

**FIGURE 17A**

1 CACCATCTCGGTTTAAGATAAAGATAATGGAGCTCTCCCCAAATGCTTCAACGGGCTCTT 60  
61 GTCTGTCAATGACAGTGAGTTCAAGGAGCACTTTGACCTTGAGGACCTGAACCTTACTCA 120  
121 TGAGGACCTGAGGCTGAAGTACTTGGGGCCACAGCAGGTAAACAATTTTGTCCCATCTG 180  
181 TGTCACGTACCTGTTGATCTTCGTAGTGGCACTCTGGGCAACGGGTGACCTGCACCGT 240  
241 CATCCCTGCGCCAGAAGGCAATGCACACGCCCACTTCTACCTCTTCAGTCTCGCGGT 300  
301 GTCCGATTGCTGGTGCTCCTGGTGGGCTTGCCCCCTGGAACTTTATGAGATGCAGCACAA 360  
361 TTACCCATTCCAGCTGGGTGCAGGTGGCTGTACTTCCGGATACTGCTTTTGGAGACTGT 420  
421 CTGCCCTGGCTTCAGTGCTCAATGTCACAGCCCCCTAAGTGTGGAGCGTTATGTGGCCGTGGT 480  
481 GCACCCACTCCAAGCCAAGTCTGTGATGACACGGACCCCATGTGCGCCGCATGTTGGGAGC 540  
541 CATCTGGGTCTTCGCTATTCTCTTCTCTCTGCCCCAACACCAAGCTTACATGGCCCTCAGTCC 600  
601 ACTCTATGTACCCCTGCCCGGGCCGGTGCCCCGATTACGTTACGTGTACGCTGGTGCGTCC 660  
661 CCAGTTCTTCTACAAAGTTGGTAATACAGACGACCATACTGCTCTTCTTCTGTCTGCCCAT 720

## FIGURE 17B

721	GGTCACCATCAGTGTGCTGTACCTGCTCATTTGGCTGAGGCTGCGGAGGAGAGGATGTT	780
781	GCTCCAAGAGAGGTCAAGGCAGGATATCTGCAGCAGCCAGGCGCTCCACAGAAG	840
841	TATTCAGCTTCGAGATAGGGAACGCAGACAGGTGACCAAGATGCTAATGCTCTGGTTAT	900
901	AGTATTGGCACCTGCTGGGTTCCATTCCATGCTGACCGTCTCATGTGAGTATGGTGTC	960
961	CCATTGGACTGACGGCCTGCGCCTTGCCCTTCCAGTCTGTGCACCTTGCTTGGTGCTT	1020
1021	CTTGTAACCTCGGCTCAGCGGCTAACCCGGAGCTCTACAACCTCATGTCCACTCGCTTCCG	1080
1081	AGAGTCCTTCCGGGAAACCCCTGGGCCCTTGGGACACGGTGCTGTCAATCGCCACCAACCGCG	1140
1141	TCACGACTCCCATAGCCACCTTAGGTTGACCACAGTCAGCACCCCTGTGTGACAGGAACAG	1200
1201	CAGGGATGTACCCCTGGCTGAGAAACAGGGATCCAGGGTGTGAGCAAGAGACAGACCCCTCC	1260
1261	TGAATAAAATCCTGTGGCCTCACCCACAGGGC	1292

**FIGURE 18A**

1	M	E	L	S	P	N	A	S	T	G	L	S	C	N	D	S	E	F	K	20	
21	E	H	F	D	L	E	D	L	N	L	T	H	E	D	L	R	L	K	Y	L	40
41	G	P	Q	Q	V	K	Q	F	L	P	I	C	V	T	Y	L	L	I	F	V	60
61	V	G	T	L	G	N	G	L	T	C	T	V	I	L	R	Q	K	A	M	H	80
81	T	P	T	N	F	Y	L	F	S	L	A	V	S	D	L	L	V	L	L	V	100
101	G	L	P	L	E	L	Y	E	M	Q	H	N	Y	P	F	Q	L	G	A	G	120
121	G	C	Y	F	R	I	L	L	L	E	T	V	C	L	A	S	V	L	N	V	140
141	T	A	L	S	V	E	R	Y	V	A	V	V	H	P	L	Q	A	K	S	V	160
161	M	T	R	T	H	V	R	R	M	L	G	A	I	W	V	F	A	I	L	F	180
181	S	L	P	N	T	S	L	H	G	L	S	P	L	Y	V	P	C	R	G	P	200
201	V	P	D	S	V	T	C	T	L	V	R	P	Q	F	F	Y	K	L	V	I	220
221	Q	T	T	I	L	L	F	F	C	L	P	M	V	T	I	S	V	L	Y	L	240

FIGURE 18B

241	<u>L I G L</u>	R R L R R	E R M L L	Q E E V	K G R	260
261	I S A A	A R Q A S	H R S I Q	L R D R	E R	280
281	R Q V T	K M L I A	L V I V	F G T C	W V P	300
301	<u>F H A</u>	D R L M W	S M V S H	W T D G	L R L	320
321	A F Q S	V H L A S	G V F L	Y L G S	A A N	340
341	<u>P E L Y</u>	N L M S T	R F R E	S F R E	T L G	360
361	L G T R	C C H R H	Q P R H	D S H S	H L R	380
381	L T T V	S T L C D	R N S R	D V P L	A E N	400
401	R D P G	C E Q E	T D P P	E		413

## FIGURE 19A

1 GGGACAGCACGTTAGACCCAAAGTCTCATGGACTTCCTCTCTCAGTGTCATTTTTCTCA 60  
61 TCTGTAAATGGGATTGTTGTCCAGAAAAAGGAGACATTCTCAGCTTCGGCTCTCCCCAA 120  
121 ATGCTTCAACGGGCTCTTGTCCTGCAATGACAGTGAGTTCAAGGAGCACTTTGACCTTG 180  
181 AGGACCTGAACCTTACTCATGAGGACCTGAGGCTGAAGTACTTGGGGCCACAGCAGGTAA 240  
241 AACAAATTTTGCCCATCTGTGTCACGTACCCTGTTGATCTTCGTAGTGGGCACTCTGGGCA 300  
301 ACGGGTTGACCTGCACCGTCACTCCTGCGCCAGAAAGGCAATGCCACACGCCCACTTCT 360  
361 ACCTCTTCAGTCTCGCGGTGTCCGATTTGCTGGTGCTCCTGGTGGGCTTGCCCCCTGGAAC 420  
421 TTTATGAGATGCAGCACAAATTACCCATTCCAGCTGGGTGCAGGTGGCTGTACTTCCGGA 480  
481 TACTGCTTTTGGAGACTGTCTGCCCTGGCTTCAGTGCTCAATGTCAAGCCCTAAGTGTGG 540  
541 AGCGTTATGTGGCCCGTGGTGCACCCCACTCCAAGCCAAGTCTGTGATGACACGGACCCATG 600  
601 TCGCGCCGCATGTGGGAGCCATCTGGGTCTTCGCTATTCTCTCTCTGCCCCAACACCA 660  
661 GCTTACATGGCCCTCAGTCCACTCTATGTACCCCTGCCGGGGCCGGTGCCCGATTTCAGTTA 720

## FIGURE 19B

721	CGGTACGCTGGTGGTCCCGAGTCTTCTACAAGTTGGTAATACAGACGACCATACTGC	780
781	TCTTCTTCTGTCTGCCCATGGTCACCATCAGTGTGCTGTACCTGCTCATTTGGGCTGAGGC	840
841	TGCGGAGGAGAGGATGTTGCTCCAAGAGGAGGTCAAGGCAGGATATCTGCAGCAGCCA	900
901	GGCAGGCCCTCCACAGAAGTATTACGCTTCGAGATAGGGAACGCAGACAGGTGACCAAGA	960
961	TGCTAATTGCTCTGGTTATAGTATTGGCACCTGCTGGGTTCCATTCCATGCTGACCGTC	1020
1021	TCATGTGGAGTATGGTGTCCCATTTGGACTGACGGCCTGCGCCTTCCAGTCTGTGC	1080
1081	ACCTTGCTTCTGGTGTCTTCTTGTAACCTCGGCTCAGCGGCTAACCCGGAGCTCTACAACC	1140
1141	TCATGTCCACTCGCTTCCGAGAGTCCCTTCCGGGAAACCCCTGGGCCCTTGGGACACGGTGCT	1200
1201	GTCAATCGCCCAACCCGGTCAACGACTTCCCATAGCCACCTTAGGTTGACCACAGTCAAGCA	1260
1261	CCCTGTGTGACAGGAACAGCAGGGATGTACCCCTGGCTGAGAAACAGGGATCCAGGGTGTG	1320
1321	AGCAAGAGACAGACCCCTCCTGAATAAAATCCTGTGGCCTCACCCACAGGGC	1371

FIGURE 20A

1	M	D	F	L	S	Q	C	H	F	F	L	I	C	K	M	G	L	S	R	20
21	K	R	R	H	S	Q	L	R	L	S	P	N	A	S	T	G	L	S	C	40
41	N	D	S	E	F	K	E	H	F	D	L	E	D	L	N	L	T	H	E	60
61	L	R	L	K	Y	L	G	P	Q	Q	V	K	Q	F	L	P	I	C	V	80
81	<u>Y</u>	<u>L</u>	<u>L</u>	<u>I</u>	<u>F</u>	<u>V</u>	<u>V</u>	<u>G</u>	<u>T</u>	<u>L</u>	<u>G</u>	<u>N</u>	<u>G</u>	<u>L</u>	<u>T</u>	<u>C</u>	<u>T</u>	<u>V</u>	<u>I</u>	100
101	R	Q	K	A	M	H	T	P	T	N	F	Y	L	F	S	L	A	V	S	120
121	<u>L</u>	<u>L</u>	<u>V</u>	<u>L</u>	<u>L</u>	<u>V</u>	<u>G</u>	<u>L</u>	<u>P</u>	<u>L</u>	<u>E</u>	L	Y	E	M	Q	H	N	Y	140
141	F	Q	L	G	A	G	G	C	Y	F	R	I	L	L	L	E	T	V	C	160
161	<u>A</u>	<u>S</u>	<u>V</u>	<u>L</u>	<u>N</u>	<u>V</u>	<u>T</u>	<u>A</u>	<u>L</u>	<u>S</u>	<u>V</u>	E	R	Y	V	A	V	V	H	180
181	L	Q	A	K	S	V	M	T	R	T	H	V	R	R	M	L	G	A	I	200
201	<u>V</u>	<u>F</u>	<u>A</u>	<u>I</u>	<u>L</u>	<u>F</u>	<u>S</u>	<u>L</u>	<u>P</u>	<u>N</u>	<u>T</u>	<u>S</u>	L	H	G	L	S	P	L	220
221	V	P	C	R	G	P	V	P	D	S	V	T	C	T	L	V	R	P	Q	240



## FIGURE 20B

241	F	Y	K	L	V	I	Q	T	T	I	L	L	F	F	C	L	P	M	V	T	260
261	I	S	V	L	Y	L	L	I	G	L	R	L	R	R	E	R	M	L	L	Q	280
281	E	E	V	K	G	R	I	S	A	A	A	R	Q	A	S	H	R	S	I	Q	300
301	L	R	D	R	E	R	R	Q	V	T	K	M	L	I	A	L	V	I	V	F	320
321	G	T	C	W	V	P	F	H	A	D	R	L	M	W	S	M	V	S	H	W	340
341	T	D	G	L	R	L	A	F	Q	S	V	H	L	A	S	G	V	F	L	Y	360
361	L	G	S	A	A	N	P	E	L	Y	N	L	M	S	T	R	F	R	E	S	380
381	F	R	E	T	L	G	L	G	T	R	C	C	H	R	H	Q	P	R	H	D	400
401	S	H	S	H	L	R	L	T	T	V	S	T	L	C	D	R	N	S	R	D	420
421	V	P	L	A	E	N	R	D	P	G	C	E	Q	E	T	D	P	P	E		439

FIGURE 21A

Rat SNORF62a	~~~~~	~~~~~	~~~~~MELS	PNASTGLLSC	NDSEFKEHFD
Rat SNORF62b	MDFLSQCHFF	LICKMGLLSR	KRRHSQRLRS	PNASTGLLSC	NDSEFKEHFD
Hum SNORF62	~~~~~	~~~~~	~~~~~MTPCL	NCSVLPGLDY	PGGARNPMAC
				NGSAARGHFD	
Rat SNORF62a	LEDNLTHED	LRLKYLGPQQ	VKQFLPICVT	YLLIFVVGTL	GNGLTCTVIL
Rat SNORF62b	LEDNLTHED	LRLKYLGPQQ	VKQFLPICVT	YLLIFVVGTL	GNGLTCTVIL
Hum SNORF62	PEDNLTDEA	LRLKYLGPQQ	TELFMPICAT	YLLIFVVGAV	GNGLTCLVIL
Rat SNORF62a	RQKAMHTPTN	FYLFSLAVSD	LLVLLVGLPL	ELYEMQHNYP	FQLGAGGCYF
Rat SNORF62b	RQKAMHTPTN	FYLFSLAVSD	LLVLLVGLPL	ELYEMQHNYP	FQLGAGGCYF
Hum SNORF62	RHKAMRTPTN	YYLFSLAVSD	LLVLLVGLPL	ELYEMWHNYP	FLLGVGGCYF
Rat SNORF62a	RILLETVCL	ASVLNVTALS	VERYVAVVHP	LQAKSVMTRT	HVRRMLGAIW
Rat SNORF62b	RILLETVCL	ASVLNVTALS	VERYVAVVHP	LQAKSVMTRT	HVRRMLGAIW
Hum SNORF62	RTLLEFEMVCL	ASVLNVTALS	VERYVAVVHP	LQARSMVTRA	HVRRVLGAVW

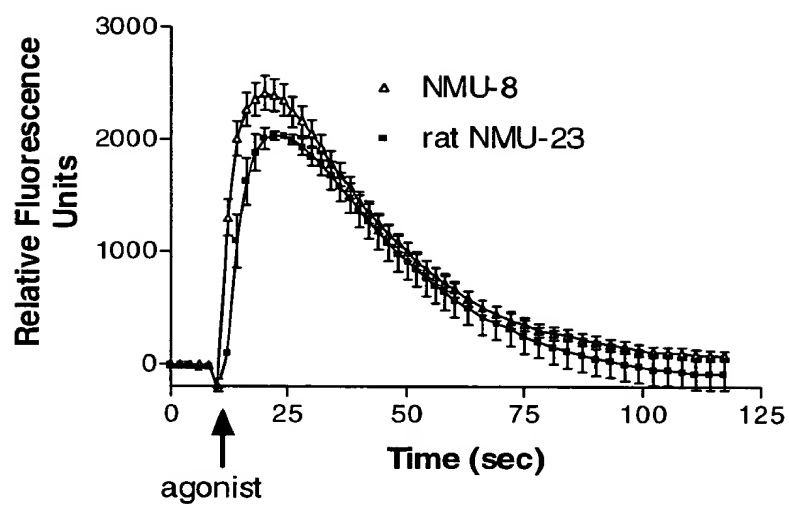
FIGURE 21B

Rat SNORF62a	VFAILFSLPN	TSLHGLSPLY	VPCRGVPVPS	VTCTLVRPQF	FYKLVIQTTI
Rat SNORF62b	VFAILFSLPN	TSLHGLSPLY	VPCRGVPVPS	VTCTLVRPQF	FYKLVIQTTI
Hum SNORF62	GLAMLCSLPN	TSLHGIRQLH	VPCRGVPVPS	AVCMLVRPRA	LYNMVVQTTA
Rat SNORF62a	LLFFCLPMVT	ISVLYLLIGL	RLRRERMLLQ	EEVKGRISAA	ARQASHRSIQ
Rat SNORF62b	LLFFCLPMVT	ISVLYLLIGL	RLRRERMLLQ	EEVKGRISAA	ARQASHRSIQ
Hum SNORF62	LLFFCLPMAI	MSVLYLLIGL	RLRRERLLLM	QEAKGRGSAA	ARSRYTCRLQ
Rat SNORF62a	LRDRERRQVT	KMLIALVIVF	GTCWVPFHAD	RLMWSMVSHW	TDGLRLAFQS
Rat SNORF62b	LRDRERRQVT	KMLIALVIVF	GTCWVPFHAD	RLMWSMVSHW	TDGLRLAFQS
Hum SNORF62	QHDRGRRQVT	KMLFVLVVVF	GICWAPFHAD	RVMWSVVSQW	TDGLHLAFQH
Rat SNORF62a	VHLASGVFLY	LGSAAANPELY	NLMSTRFRES	FRETGLGLTR	CCHRHQPRHD
Rat SNORF62b	VHLASGVFLY	LGSAAANPELY	NLMSTRFRES	FRETGLGLTR	CCHRHQPRHD
Hum SNORF62	VHVISGIFFY	LGSAAANPVLY	SLMSSRFRET	FQEALCLGA.	CCHRLRPRHS

FIGURE 21C

Rat SNORF62a	SHSHLRLLTTV	STLCDRNSRD	V...PLAENR	DPGCEQETDP	PE
Rat SNORF62b	SHSHLRLLTTV	STLCDRNSRD	V...PLAENR	DPGCEQETDP	PE
Hum SNORF62	SHSLSRMTTG	STLCDVGSLG	SWVHPLAGND	GPEAQQETDP	S~~

FIGURE 22



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**FIGURE 23**